REMARKS

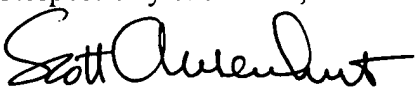
In accordance with 37 C.F.R. §§1.821 to 1.825, Applicants request entry of this amendment. This amendment is accompanied by a floppy disk containing SEQ ID NOS:1-48, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



Scott L. Ausenhus
Reg. No. 42, 271

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (415) 576-0200
Fax: (415) 576-0300
SLA:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 19 of page 3 has been amended as follows:

Figure 1A shows the polynucleotide sequence of the VHL/E US28 coding sequence (SEQ ID NO:3) ~~(SEQ ID NO:1)~~ and Figure 1B shows the amino acid sequence for the corresponding VHL/E US28 polypeptide (SEQ ID NO:4) ~~(SEQ ID NO:2)~~. The extracellular domain is underlined.

Paragraph beginning at line 22 of page 3 has been amended as follows:

Figure 2 is a sequence comparison of the amino acid sequences for human US28 (AD169) (upper sequence; SEQ ID NO:48), rhesus US28.1 (second sequence; SEQ ID NO:6), rhesus US28.2 (third sequence; SEQ ID NO:8), rhesus US28.3 (fourth sequence; SEQ ID NO:10), ~~rhesus US28.3 (fourth sequence),~~ rhesus US28.4 (fifth ~~fourth~~ sequence; SEQ ID NO:12) and rhesus US28.5 (bottom sequence; SEQ ID NO:14). Regions of sequence similarity are indicated in the boxed regions as determined using the sequence comparision program, SeqVu, from the Garvan Institute, Sydney, Australia. Shaded regions correspond to regions of similar hydrophilicity or hydrophobicity as determined by the SeqVu program.

Paragraph beginning at line 29 of page 3 has been amended as follows:

Figure 3 is a sequence comparison of the amino acid sequences for human UL78 [strain AD169 (Genebank Accession # X17403, see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence; SEQ ID NO:16) and rhesus

UL78 (lower sequence; SEQ ID NO:18). Regions of sequence similarity are indicated in the boxed regions as determined using the comparision program SeqVu, from the Garvan Institute, Sydney, Australia, with shaded regions corresponding to regions of similar hydrophilicity or hydrophobicity as determined by the same program.

Paragraph beginning at line 3 of page 4 has been amended as follows:

Figure 4 is a sequence comparison of the amino acid sequences for human UL33 [Genebank Accession # X17403; see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence; SEQ ID NO:20), human UL33 spliced (second sequence; SEQ ID NO:22), rhesus UL33 (third sequence; SEQ ID NO:24) and rhesus UL33 spliced (lower sequence; SEQ ID NO:26). Regions of sequence similarity are indicated in the boxed regions as determined using the comparision program SeqVu, from the Garvan Institute, Sydney, Australia; regions of similar hydrophilicity or hydrophobicity as determined by the same program are shaded.

Paragraph (Table 4) beginning at line 7 of page 27 has been amended as follows:

Table 4: Primer sequences for amplifying rhUS28 homologs.

rhUS28 Homolog	**Primer Sequence (Upper Strand)**	**SEQ ID NO:**	**Primer Sequence (Lower Strand)**	**SEQ ID NO:**
rhUS28.1 ~~rh28.1~~	TATGAATAACACATCTTGCAACTTC	28	CACACAGACCACATGTAC	29
rhUS28.2 ~~rh28.2~~	ATTCAACATGACCAACGCCGG	30	GCATTTCCGTGGATTCG	31
rhUS28.3 ~~rh28.3~~	CATGACCAACACTAAC	32	GAGTCTTTTGTGAGCC	33
rhUS28.4 ~~rh28.4~~	TATGAATTCGAGCCAGCAC	34	GTACGCGACTAAGACAGAG	35
rhUS28.5 ~~rh28.5~~	AAAGATGACTACCACCAC	36	ATAACCTAGCACCTCCCC	37
rhUL78 ~~rh78~~	CTGAAACCATGATTACGG	38	CACGCAGCACAAGAGCAC	39
rhUL33 ~~rh33~~	CATGACCAATCTTTACTC	40	GTGTCGCCACTCCTACCC	41
rhUL33 spliced ~~rh33 spliced~~	AAGTTAGTGATGGCAGTC	42	GTATGTAAACCCGTGGAG	43

Paragraph beginning at line 11 of page 35 has been amended as follows:

Typically, the antisense polynucleotides used in the methods comprise an antisense sequence of typically at least about 10 contiguous nucleotides, in other instances at least 12 or 14 contiguous nucleotides, and in still other instances up to about 100 contiguous nucleotides that specifically hybridize to a sequence from a mRNA encoding US28 or a US28 homolog in the target organism. Thus, in the treatment of infections caused by human strains of CMV, appropriate polynucleotides sequences can be prepared based upon the nucleotide sequence for human US28 as set forth in SEQ ID NO:3 ~~SEQ ID NO:1~~ (FIG. 1A) and for human UL33 (SEQ ID NO:19), human UL33 spliced (SEQ ID NO:21) and human UL78 (SEQ ID NO:15). Likewise, in the treatment of infections caused by rhesus strains, appropriate polynucleotides can be prepared based

upon the nucleotide sequences for the various rhesus US28 homologs as shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.

Paragraph beginning at line 9 of page 36 has been amended as follows:

Ribozymes are also useful for inhibiting US28 or US28 homolog activity in an animal. Useful ribozymes can comprise 5'- and 3'-terminal sequences complementary to the US28 mRNA or US28 homolog mRNA and can be engineered by one of skill on the basis of the US28 mRNA sequence (see, e.g., SEQ ID NO:3 ~~SEQ ID NO:1~~; see FIG. 1A) and US28 homolog sequences disclosed herein (SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25). Ribozymes that can be utilized in the treatment methods include those having characteristics of group I intron ribozymes (Cech, 1995, *Biotechnology* 13:323) and others of hammerhead ribozymes (Edgington, 1992, *Biotechnology* 10:256).

Paragraph beginning at line 5 of page 37 has been amended as follows:

Antibodies are an example of one type of agent that can be used to inhibit binding between a chemokine and US28 or a US28 homolog. Such inhibition can be achieved, for example, through steric hindrance. Typically, the antibody specifically binds an epitope on the extracellular region of US28 (e.g., SEQ ID NO:4 ~~SEQ ID NO:1~~; see FIG. 1B) or one of the US28 homologs. Thus, certain treatments involve administering an antibody that specifically binds to human UL33 (SEQ ID NO:20) ~~(SEQ ID NO:19)~~, human UL33 spliced (SEQ ID NO:22) ~~(SEQ ID NO:33)~~ or human UL78 (SEQ ID NO:16) ~~(SEQ ID NO:15)~~. Other treatment methods involve administering an antibody that specifically binds to one of the rhesus US28 homologs (i.e., SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26).

Paragraph beginning at line 33 of page 38 has been amended as follows:

The vaccines are generally designed to include CMV or some portion of the virion in which US28 or US28 homolog has been disabled such that US28 or US28 protein is either not produced or is produced in inactive form. In some instances, this means that the segment of the genome encoding US28 or US28 homolog has been completely or substantially removed, either chemically, enzymatically or via recombination. Specific segments, or at least portions thereof, that can be removed for HCMV include those regions of the genome corresponding to US28 (SEQ ID NOS:1 and 3), UL33 (SEQ ID NO:19), UL33 spliced (SEQ ID NO:21) and UL78 (SEQ ID NO:15) ~~(SEQ ID NO:17)~~. For rhCMV, segments, or portions thereof, that can be removed include SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25~~)~~.

Paragraph beginning at line 24 of page 43 has been amended as follows:

A list of the sequence identifiers for the nucleotide sequences of the open reading frames encoding the rhesus US 28 homologs and the corresponding amino acid sequences are summarized in Table 3 *supra*. The actual nucleotide and amino acid sequences of the rhesus US28 homologs are shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25 (nucleotide sequences) and SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26 ~~6, 8, 10, 12, 14, 18, 24 and 26~~ (amino acid sequences).